

Sampling structure and diversity of old-growth forests in the Pacific Northwest: Effect of plot size

Andrew N. Gray

Forest Inventory and Analysis Program, Portland OR



Introduction

Information is needed about the regional distribution and trends of forest habitat and diversity to meet national and international objectives. The Forest Inventory and Analysis program, with one field plot per 2,400 ha of forestland across the nation, plays a key role in providing accurate data on forest conditions. A primary need for most land-owners in the coastal Pacific Northwest is information on the extent and rate of development of old-growth forest structure. Old-growth stands are important habitat for a variety of plants, animals, lichens, and fungi. In addition, old-growth structures in younger stands, like remnant large trees, snags, and down logs, significantly enhance forest composition and function. For example, large conifer trees growing in riparian zones are believed to be critical to providing large wood to structure stream habitat for salmonids.

Although a variety of plot designs and sizes have been used to sample old-growth forest attributes, few analyses of the effect of plot design on the accuracy of results are available. Stand-level ecological objectives often involve determining tree size distribution and species composition (Max et al. 1996). The objective of this study was to determine the effect of different plot sizes on estimating the density of large live and dead trees, and species richness. Existing intensive plot data was analyzed in a framework compatible with current inventory plot design (Figure 1).

Figure 1: Forest Inventory and Analysis plot

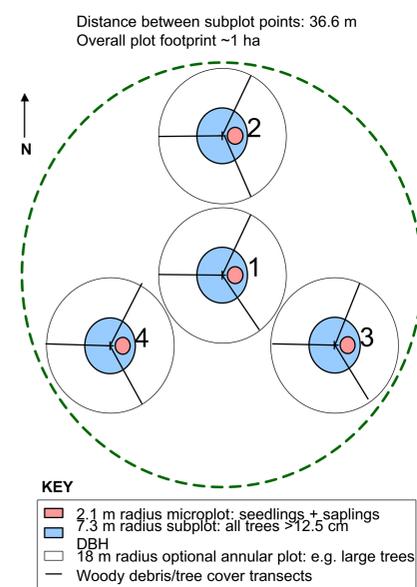


Table 1: Characteristics of stem-mapped reference stands used for placement of imaginary plots of different sizes. The first three stands are referred to as "mature", the last nine as "old-growth".

stand	plot ha	duration yrs	stand age yrs	mean DBH (cm)	dominant species	plant community type	trees >122 cm (n/ha)
RS37	1.00	17	130	51.1	psme,acma	tshe/acci/pomu	1.0
RS35	2.00	16	130	40.7	psme,alru	tshe/acci/pomu	1.0
RS24	1.00	17	90	45.9	psme,tshe	tshe/oxor	0.0
RS01	1.00	15	460	44.0	psme,acma	psme/hodi	14.0
RS02	1.00	15	460	54.3	psme,tshe	tshe/bene	23.0
RS29	1.00	17	450	75.3	psme,thpl	tshe-acci/pomu	42.0
RS31	1.00	17	450	55.4	psme,tshe	tshe-abam/bene	28.0
RS30	1.00	17	450	76.0	psme,thpl	tshe-abam/rhna-libo	35.0
RS03	1.00	17	460	50.3	psme,thpl	tshe-abam/rhna-libo	24.0
RS23	1.00	16	450	57.4	tshe,psme	abam/vaal/coca	7.0
RS34	2.00	16	450	51.2	thpl,psme	tshe/acci/pomu	24.5
TO04	1.00	20	750	51.1	psme,tshe	tshe/opho	13.0



Methods

The analysis used spatially explicit tree data from intensive research and inventory plots and simulated different plot sizes to "sample" trees and calculate density and richness. Most of the analysis used data from 13 mapped, ~homogeneous, hectare-sized plots (Acker et al. 1998), in which all trees ≥15 cm DBH (diameter at breast height, 1.37 m) were measured. Most stands were dominated by Douglas-fir (*Pseudotsuga menziesii*); three were 90-130 yrs old ("mature"), and the rest were >400 yrs old ("old-growth"; Table 1). Tree species richness ranged from 5 to 8 (Table 2). Most stands had at least one rare species (i.e. that represented less than 10% of the stems present), and one had six (stand TO04).

Trees were placed into four size classes for the analyses: 15-33, 33-75, 75-122, and ≥122 cm DBH. The response variables of interest were:

- * tree density by size class,
- * density of tree mortality by size class, and
- * tree species richness by size class.

Simulated circular subplots were randomly placed within each stand (Figure 2). Plot sizes ranged from 2 to 25 m in radius, in 2 m increments. Subplot centers were constrained to keep samples within plot boundaries. Every 4 subplots were grouped into a virtual "plot" sample. Since subplots were placed independently, subplots within some groups overlapped somewhat, particularly for larger subplot sizes. Thirty virtual "plots" per hectare were created for each stand and subplot size.

Response variables were calculated for each plot, and the "sample error" calculated as the percent difference between the sample estimate and the actual full-stand ("true") value as:

$$\text{error}_{ijk} = |x_{ijk} - u_{jk}| / u_{jk}$$

where i = subplot size, j = tree size class, and k = stand. Sample errors for each stand were then averaged to derive the "mean sample error". The distribution of the mean sample errors in this study were roughly comparable to that of the standard deviation: of 20,760 deviations calculated for tree density, 59.3% were less than or equal to the mean (standard deviation contains 66% of the observations for a normal distribution).

The choice of the diameter limit for defining "large" trees and snags was investigated using the same approach as above, but using only 2 plot sizes and varying the diameter limit for trees sampled between 35 and 125 cm in increments of 10 cm.

The applicability of these results beyond the 13 reference stands used was investigated by subsampling trees using 2 plot sizes from 285 BLM inventory plots in western Oregon.

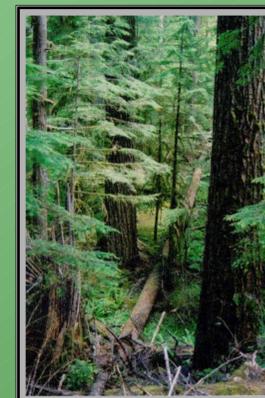
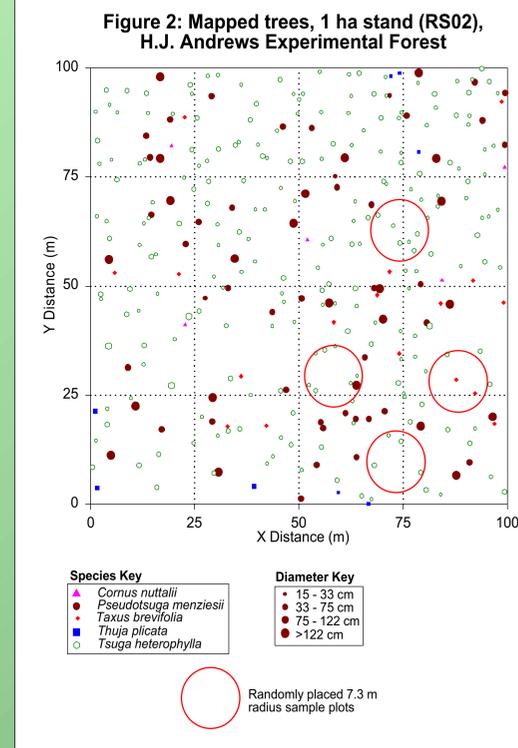


Table 2: Density of different tree species (#/ha) and total species richness in stem-mapped reference stands.

	RS37	RS35	RS24	RS01	RS02	RS29	RS31	RS30	RS03	RS23	RS34	TO04
<i>Abies amabilis</i>						1	5	5	37	40	2	44
<i>Abies concolor</i>										13		
<i>Abies grandis</i>												7
<i>Acer macrophyllum</i>	46	33		27							5	
<i>Alnus rubra</i>	36	30	9									1
<i>Arbutus menziesii</i>				3								
<i>Castanopsis chrysophylla</i>			1						5			
<i>Calocedrus decurrens</i>				1								
<i>Cornus nuttallii</i>	4	24	5	6	6						5	
<i>Pinus lambertiana</i>				1								
<i>Pinus monticola</i>										2		
<i>Pseudotsuga menziesii</i>	112	202	292	387	64	34	57	45	27	25	16	6
<i>Rhamnus purshiana</i>	18	49										
<i>Taxus brevifolia</i>	10	6	4	26	34	23	11	40	49	39	57	5
<i>Thuja plicata</i>		1	1		13	84	10	47	84	14	90	18
<i>Tsuga heterophylla</i>	10	34	31	7	260	125	294	122	272	125	208	234
<i>Tsuga mertensiana</i>									1			1
Total	236	377	343	458	377	267	377	259	476	258	382	316
Species richness	7	8	7	8	5	5	5	5	8	7	7	8

Results: plot size

Tree density

Sample error dropped rapidly with increasing subplot size for all tree size classes in all stands (Figure 3). Error tended to level off between subplot radii of 14 to 16 m, where mean sample error ranged between 20 and 30% (except for trees ≥122 cm DBH in mature stands, which were present at very low density). Sample error does not fall towards zero with the largest plot sizes because randomly-placed large plots double-sampled some portions of stands, and some portions of square or rectangular stands were not sampled by large circular subplots.

Mortality

The sample error for measuring tree mortality rates (even over sample periods of 16-20 yrs) was substantially greater than the error for tree density. Sample error also dropped rapidly with increasing subplot size but showed less of a tendency to level off, except perhaps above subplot radii of 20 m (Figure 4). At this subplot size, mean sample error was about 30% and 50% for trees less than 75 cm DBH, in mature and old-growth stands, respectively. For trees over 75 cm DBH, mean percent deviation of this subplot size was about 100% and 80% in mature and old-growth stands, respectively.

Species richness

Sampling error of species richness decreased with increasing tree size class, reflecting trends in actual richness (Figure 5). In mature stands, mean errors declined with increasing subplot size for trees less than 75 cm DBH, leveling off between 20 and 22 m radius. Mature stand error curves were relatively flat above a subplot radius of 8 m for trees >75 cm DBH. In old-growth stands, error curves for all tree size classes tended to level off at subplot sizes of around 20 m radius.

Figure 3: error for density between sample and stand; by stand type, plot size, and tree diameter class

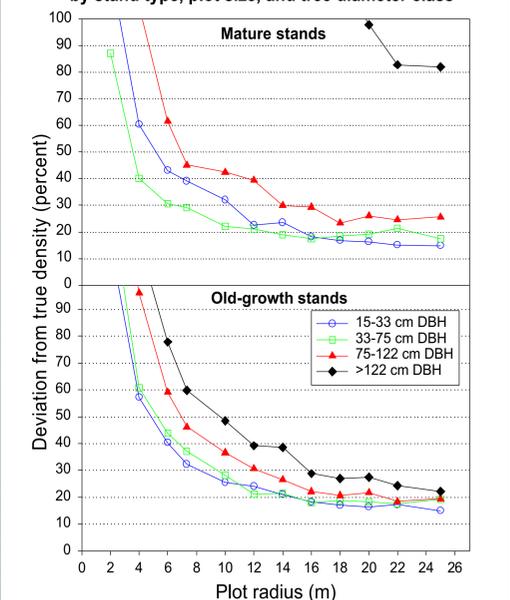


Figure 4: error in mortality between sample and stand; by stand type, plot size, and tree diameter class

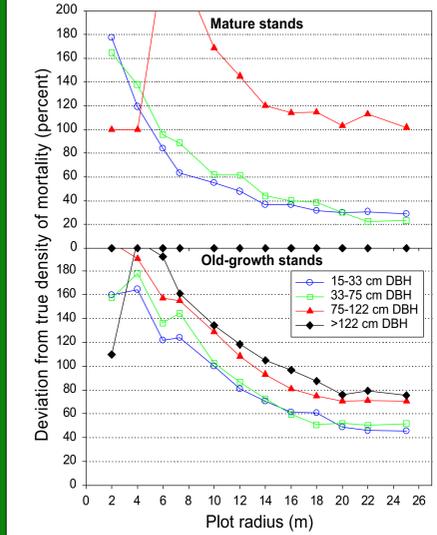
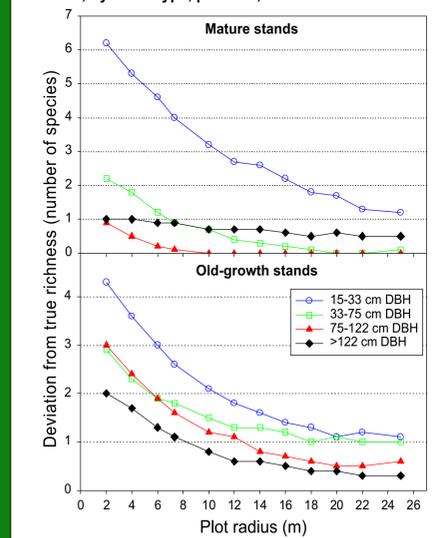


Figure 5: error in species richness between sample and stand; by stand type, plot size, and tree diameter class



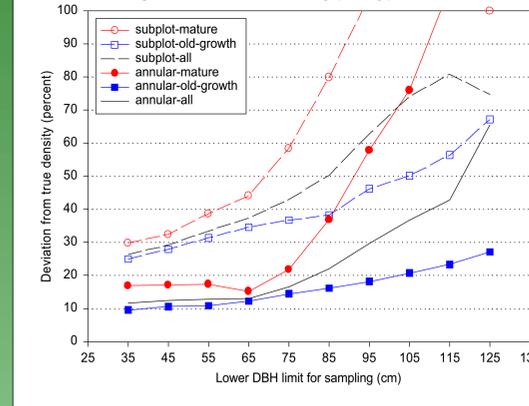
Results: diameter cutoff for "large" trees

This analysis explored the effect of the diameter criteria for sampling trees on the FIA annular subplot (Figure 1). In other words, for trees greater than DBH=x, what is the gain in accuracy from using the 18 m radius annular subplot instead of the 7.3 m radius subplot?

Sample errors increased with increasing diameter limit because of lower densities of trees above each DBH, particularly for the mature stands (Figure 6). Errors from the smaller subplot size tended to increase more rapidly above 65-85 cm DBH. The mean error for the smaller subplot size crosses the 50% point at 85 cm—that is, on average, the estimated density of trees ≥ 85 cm is off by 50% from the true density. These lines of evidence suggest it might be reasonable to rely on the on the larger annular plot for sampling trees greater than ~75 cm DBH.



Figure 6: error between sample and stand density of trees above given diameter limits; by plot type and stand size



Results: plot size effects on a wide range of forest types

The analysis of data from the systematic BLM inventory, which sampled a wide range of stand age and composition in western Oregon, confirmed the earlier results from the mapped stands. Estimated densities of large trees using 7.3 m radius subplots were highly variable (Figure 7). For example, on plots were estimated density from the 18 m radius subplots ranged from 20-30 per ha, densities from the smaller subplots ranged from 0 to 60 trees per ha.

Similar results were obtained for standing dead trees ("snags") (Figure 8). For example, on plots were estimated density from the 18 m radius subplots ranged from 5-10 per ha, densities from the smaller subplots ranged from 0 to 30 snags per ha.

Figure 7: Distribution of estimated density of trees ≥ 75 cm DBH on 7.3 m subplots, vs density sampled with 18 m annular plots (BLM data, N=285)

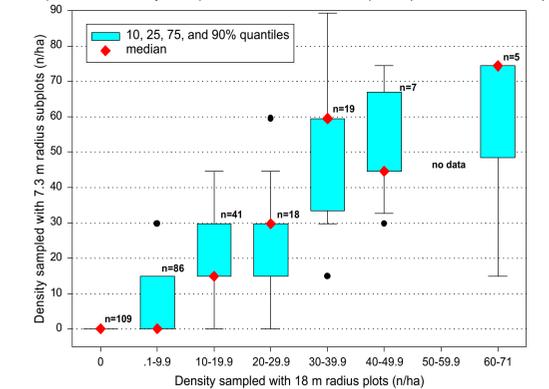
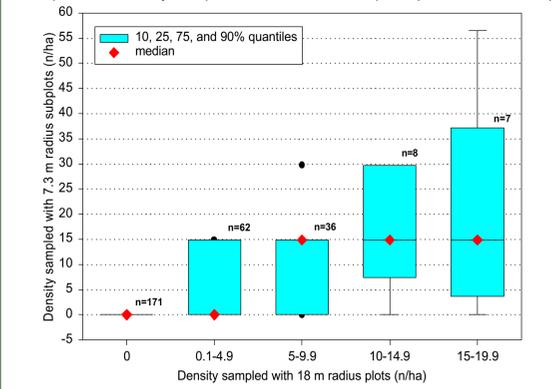


Figure 8: distribution of estimated density of snags >75 cm DBH on 7.3 m subplots, vs density sampled with 18 m annular plots (BLM data, N=285)



Discussion

This study indicates that accurately determining the density of large trees and snags on forest inventory plots will require an augmentation of the standard FIA design. The 18 m radius annular subplot appears to be adequate for a range of forest types. The diameter criteria for "large" trees could be determined by management objectives (e.g. old growth criteria for different forest types).

Accurately determining species richness in natural stands is not possible with a clustered, nested-subplot-size design. This suggests that relying on these plots to describe factors affecting stand-level species diversity (e.g. Stapanian et al. 1997) is prone to error.

The limitations of this study grow out of its strengths. The stem-mapped stands were subjectively placed in more or less homogeneous stands, which allows in-depth examination of a population of interest, but would result in a higher density of large trees than would be found on most systematically-placed plots. Subjective placement also raises the possibility that stands were exemplary rather than typical (i.e. particularly large trees or high species diversity). These real and potential drawbacks, if true, would lead one to choose a smaller subplot size than necessary for tree density (because true density would be lower) and a larger subplot size than necessary for species richness (because true richness would be lower). Also, the more realistic test using data from systematically-placed western Oregon BLM plots tends to confirm the results from the stem-mapped stands.

Managing for late-successional and old-growth attributes has become an important emphasis for many federal and state forest managers in the region. The primary criteria for Douglas-fir old-growth in the region is 20 trees per hectare ≥ 100 cm or >200 yrs in age (Old Growth Definition Task Group 1986). With four 7.32 m radius subplots having a per-tree density expansion factor of 14.9 trees per hectare, it would be unwise to expect these plots to be able to determine whether a stand was old-growth unless several trees were sampled (i.e. a very dense old-growth stand). Four annular plots 18 m in radius have an expansion factor 2.5 trees per hectare, greatly enhancing the ability to determine the abundance of large trees and snags.

References

- Acker, S.A., W.A. McKee, M.E. Harmon, and J.F. Franklin. 1998. Long-term research on forest dynamics in the Pacific Northwest: a network of permanent plots. Pp. 93-106 in F. Dallmeier and J.A. Comiskey, eds. Forest biodiversity in North, Central and South America, and the Caribbean: Research and monitoring. UNESCO, Paris.
- Max, Timothy A., Schreuder, Hans T., Hazard, John W., Oswald, Daniel D., Tepley, John, and Alegria, Jim. 1996. The Pacific Northwest region vegetation and inventory monitoring system. USDA Forest Service Research Paper PNW-493.
- Old Growth Definition Task Group. 1986. Interim definitions for old-growth Douglas-fir and mixed-conifer forests in the Pacific Northwest and California. USDA Forest Service Research Note PNW-447.
- Stapanian, Martin A., Cassell, David L., and Cline, Steven P. 1997. Regional patterns of local diversity of trees: associations with anthropogenic disturbance. Forest Ecology and Management 93: 33-44.

Acknowledgements

Data for this study was generously provided by the H.J. Andrews LTER Permanent Sample Plot group (funded by NSF and USDA Forest Service) and by USDI Bureau of Land Management, Oregon office. Support for this study was provided by the USDA Forest Service, PNW Research Station, Forest Inventory and Analysis program.

